```
   1 GTCTCGTGTA TGGCGTGGTT AAGGTTGCAG CCTCTCACCT CTGCCTTCCT
  51 CCATTTTGGG CTGGTTACCT TTGTGCTCTT CCTGAATGGT CTTCGAGCAG
 101 AGGCTGGTGG CTCAGGGGAC GTGCCAAGCA CAGGGCAGAA CAATGAGTCC
 151 TGTTCAGGGT CATCGGACTG CAAGGAGGGT GTCATCCTGC CAATCTGGTA
 201 CCCGGAGAAC CCTTCCCTTG GGGACAAGAT TGCCAGGGTC ATTGTCTATT
 251 TTGTGGCCCT GATATACATG TTCCTTGGGG TGTCCATCAT TGCTGACCGC
 301 TTCATGGCAT CTATTGAAGT CATCACCTCT CAAGAGAGGG AGGTGACAAT
 351 TAAGAAACCC AATGGAGAAA CCAGCACAAC CACTATTCGG GTCTGGAATG
 401 AAACTGTCTC CAACCTGACC CTTATGGCCC TGGGTTCCTC TGCTCCTGAG
 451 ATACTCCTCT CTTTAATTGA GGTGTGTGGT CATGGGTTCA TTGCTGGTGA
 501 TCTGGGACCT TCTACCATTG TAGGGAGTGC AGCCTTCAAC ATGTTCATCA
 551 TCATTGGCAT CTGTGTCTAC GTGATCCCAG ACGGAGAGAC TCGCAAGATC
 601 AAGCATCTAC GAGTCTTCTT CATCACCGCT GCTTGGAGTA TCTTTGCCTA
 651 CATCTGGCTC TATATGATTC TGGCAGTCTT CTCCCCTGGT GTGGTCCAGG
 701 TTTGGGAAGG CCTCCTCACT CTCTTCTTCT TTCCAGTGTG TGTCCTTCTG
 751 GCCTGGGTGG CAGATAAACG ACTGCTCTTC TACAAATACA TGCACAAAAA
 801 GTACCGCACA GACAAACACC GAGGAATTAT CATAGAGACA GAGGGTGACC
 851 ACCCTAAGGG CATTGAGATG GATGGGAAAA TGATGAATTC CCATTTTCTA
 901 GATGGGAACC TGGTGCCCCT GGAAGGGAAG GAAGTGGATG AGTCCCGCAG
 951 AGAGATGATC CGGATCCTCA AGGATCTGAA GCAAAAACAC CCAGAGAAGG
1001 ACTTAGATCA GCTGGTGGAG ATGGCCAATT ACTATGCTCT TTCCCACCAA
1051 CAGAAGAGCC GCGCCTTCTA CCGTATCCAA GCCACTCGTA TGATGACTGG
1101 TGCAGGCAAT ATCCTGAAGA AACATGCAGC AGAACAAGCC AAGAAGGCCT
1151 CCAGCATGAG CGAGGTGCAC ACCGATGAGC CTGAGGACTT TATTTCCAAG
1201 GTCTTCTTTG ACCCATGTTC TTACCAGTGC CTGGAGAACT GTGGGGCTGT
1251 ACTCCTGACA GTGGTGAGGA AAGGGGGAGA CATGTCAAAG ACCATGTATG
1301 TGGACTACAA AACAGAGGAT GGTTCTGCCA ATGCAGGGGC TGACTATGAG
1351 TTCACAGAGG GCACGGTGGT TCTGAAGCCA GGAGAGACCC AGAAGGAGTT
1401 CTCCGTGGGC ATAATTGATG ACGACATTTT TGAGGAGGAT GAACACTTCT
1451 TTGTAAGGTT GAGCAATGTC CGCATAGAGG AGGAGCAGCC AGAGGAGGGG
1501 ATGCCTCCAG CAATATTCAA CAGTCTTCCC TTGCCTCGGG CTGTCCTAGC
1551 CTCCCCTTGT GTGGCCACAG TTACCATCTT GGATGATGAC CATGCAGGCA
1601 TCTTCACTTT TGAATGTGAT ACTATTCATG TCAGTGAGAG TATTGGTGTT
1651 ATGGAGGTCA AGGTTCTGCG GACATCAGGT GCCCGGGGTA CAGTCATCGT
1701 CCCCTTTAGG ACAGTAGAAG GGACAGCCAA GGGTGGCGGT GAGGACTTTG
1751 AAGACACATA TGGGGAGTTG GAATTCAAGA ATGATGAAAC TGTGAAAACC
1801 ATAAGGGTTA AAATAGTAGA TGAGGAGGAA TACGAAAGGC AAGAGAATTT
1851 CTTCATTGCC CTTGGTGAAC CGAAATGGAT GGAACGTGGA ATATCAGATG
1901 TGACAGACAG GAAGCTGACT ATGGAAGAAG AGGAGGCCAA GAGGATAGCA
1951 GAGATGGGAA AGCCAGTATT GGGTGAACAC CCCAAACTGG AAGTCATCAT
2001 TGAAGAGTCC TATGAGTTCA AGACTACGGT GGACAAACTG ATCAAGAAGA
2051 CAAACCTGGC CTTGGTTGTG GGGACCCATT CCTGGAGGGA CCAGTTCATG
2101 GAGGCCATCA CCGTCAGTGC AGCAGGGGAT GAGGATGAGG ATGAATCCGG
2151 GGAGGAGAGG CTGCCCTCCT GCTTTGACTA CGTCATGCAC TTCCTGACTG
2201 TCTTCTGGAA GGTGCTGTTT GCCTGTGTGC CCCCCACAGA GTACTGCCAC
2251 GGCTGGGCCT GCTTCGCCGT CTCCATCCTC ATCATTGGCA TGCTCACCGC
2301 CATCATTGGG GACCTGGCCT CGCACTTCGG CTGCACCATT GGTCTCAAAG
2351 ATTCGGTCAC AGCTGTTGTT TTCGTGGCAT TTGGCACCTC TGTCCCAGAT
2401 ACGTTTGCCA GCAAAGCTGC TGCCCTCCAG GATGTATATG CAGACGCCTC
2451 CATTGGCAAC GTGACGGGCA GCAACGCCGT CAATGTCTTC CTGGGCATCG
2501 GCCTGGCCTG GTCCGTGGCC GCCATCTACT GGGCTCTGCA GGGACAGGAG
2551 TTCCACGTGT CGGCCGGCAC ACTGGCCTTC TCCGTCACCC TCTTCACCAT
2601 CTTTGCATTT GTCTGCATCA GCGTGCTCTT GTACCGAAGG CGGCCGCACC
2651 TGGGAGGGGA GCTTGGTGGC CCCCGTGGCT GCAAGCTCGC CACAACATGG
2701 CTCTTTGTGA GCCTGTGGCT CCTCTACATA CTCTTTGCCA CACTAGAGGC
2751 CTATTGCTAC ATCAAGGGGT TCTAAGCCAC AC
(SEQ ID NO: 1)

5'UTR:       1 - 9
Start Codon: 10
Stop Codon:  2773
3'UTR:       2776
```

FIGURE 1, page 1 of 2

HOMOLOGOUS PROTEINS:

Top 10 BLAST Hits:

Sequences producing significant alignments:	Score (bits)	E Value
CRA|18000005047237 /altid=gi|2498054 /def=sp|P70549|NAC3_RAT SO...	1828	0.0
CRA|18000005200270 /altid=gi|4140706 /def=gb|AAD04173.1| (AF107...	1342	0.0
CRA|1000682343796 /altid=gi|6453729 /def=gb|AAF08988.1|AF108389...	1338	0.0
CRA|18000004939788 /altid=gi|1083801 /def=pir||S43730 Na+/Ca2+-...	1335	0.0
CRA|18000005028314 /altid=gi|1279782 /def=gb|AAA97928.1| (U5266...	1334	0.0
CRA|18000004968774 /altid=gi|382752 /def=prf||1901175A Na/Ca ex...	1333	0.0
CRA|18000004882912 /altid=gi|627801 /def=pir||B53335 Na+/Ca2+-e...	1331	0.0
CRA|18000005218648 /altid=gi|4566522 /def=gb|AAD23386.1|AF10916...	1330	0.0
CRA|18000005218651 /altid=gi|4566528 /def=gb|AAD23389.1|AF10916...	1329	0.0
CRA|18000004907324 /altid=gi|479177 /def=pir||S32435 Na+/Ca2+-e...	1328	0.0

dbEST:

Sequences producing significant alignments:	Score (bits)	E Value
gi|11600765 /dataset=dbest /taxon=96...	500	e-138
gi|318815 /dataset=dbest /taxon=9606 /...	216	2e-53

EXPRESSION INFORMATION FOR MODULATORY USE:

gi|11600765 Pooled (Brain, Heart, Kidney, Lung, Spleen, Testis, Leukocyte)
gi|318815 Fetal brain

Tissue expression:

Pooled tissues (Brain, Heart, Kidney, Lung, Spleen, Testis, Leukocyte)

FIGURE 1, page 2 of 2

```
   1 MAWLRLQPLT SAFLHFGLVT FVLFLNGLRA EAGGSGDVPS TGQNNESCSG
  51 SSDCKEGVIL PIWYPENPSL GDKIARVIVY FVALIYMFLG VSIIADRFMA
 101 SIEVITSQER EVTIKKPNGE TSTTTIRVWN ETVSNLTLMA LGSSAPEILL
 151 SLIEVCGHGF IAGDLGPSTI VGSAAFNMFI IIGICVYVIP DGETRKIKHL
 201 RVFFITAAWS IFAYIWLYMI LAVFSPGVVQ VWEGLLTLFF FPVCVLLAWV
 251 ADKRLLFYKY MHKKYRTDKH RGIIIETEGD HPKGIEMDGK MMNSHFLDGN
 301 LVPLEGKEVD ESRREMIRIL KDLKQKHPEK DLDQLVEMAN YYALSHQQKS
 351 RAFYRIQATR MMTGAGNILK KHAAEQAKKA SSMSEVHTDE PEDFISKVFF
 401 DPCSYQCLEN CGAVLLTVVR KGGDMSKTMY VDYKTEDGSA NAGADYEFTE
 451 GTVVLKPGET QKEFSVGIID DDIFEEDEHF FVRLSNVRIE EEQPEEGMPP
 501 AIFNSLPLPR AVLASPCVAT VTILDDDHAG IFTFECDTIH VSESIGVMEV
 551 KVLRTSGARG TVIVPFRTVE GTAKGGGEDF EDTYGELEFK NDETVKTIRV
 601 KIVDEEEYER QENFFIALGE PKWMERGISD VTDRKLTMEE EEAKRIAEMG
 651 KPVLGEHPKL EVIIEESYEF KTTVDKLIKK TNLALVVGTH SWRDQFMEAI
 701 TVSAAGDEDE DESGEERLPS CFDYVMHFLT VFWKVLFACV PPTEYCHGWA
 751 CFAVSILIIG MLTAIIGDLA SHFGCTIGLK DSVTAVVFVA FGTSVPDTFA
 801 SKAAALQDVY ADASIGNVTG SNAVNVFLGI GLAWSVAAIY WALQGQEFHV
 851 SAGTLAFSVT LFTIFAFVCI SVLLYRRRPH LGGELGGPRG CKLATTWLFV
 901 SLWLLYILFA TLEAYCYIKG F
  (SEQ ID NO:2)
```

FEATURES:
Functional domains and key regions:
[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 4

1	45-48	NESC
2	130-133	NETV
3	135-138	NLTL
4	817-820	NVTG

---

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 2

1	378-381	KKAS
2	634-637	RKLT

---

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 11

1	113-115	TIK
2	125-127	TIR
3	597-599	TIR
4	194-196	TRK
5	267-269	TDK
6	312-314	SRR
7	460-462	TQK
8	572-574	TAK
9	594-596	TVK
10	125-127	TIR
11	597-599	TIR

---

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 16

1	69-72	SLGD
2	106-109	TSQE
3	144-147	SAPE
4	151-154	SLIE
5	277-280	TEGD
6	312-315	SRRE
7	382-385	SMSE
8	460-463	TQKE
9	522-525	TILD
10	583-586	TYGE
11	637-640	TMEE
12	672-675	TTVD
13	691-694	SWRD
14	713-716	SGEE
15	720-723	SCFD
16	794-797	SVPD

---

[5] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

Number of matches: 2

1	397-405	KVFFDPCSY
2	601-608	KIVDEEEY

---

[6] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 15

1	50-55	GSSDCK
2	422-427	GGDMSK
3	438-443	GSANAG
4	497-502	GMPPAI
5	557-562	GARGTV
6	571-576	GTAKGG
7	760-765	GMLTAI
8	774-779	GCTIGL
9	778-783	GLKDSV
10	816-821	GNVTGS
11	829-834	GIGLAW
12	831-836	GLAWSV
13	882-887	GGELGG
14	886-891	GGPRGC
15	890-895	GCKLAT

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainity
1	8	28	1.905	Certain
2	76	96	2.032	Certain
3	133	153	1.009	Certain
4	169	189	1.943	Certain
5	206	226	2.118	Certain
6	231	251	2.072	Certain
7	505	525	0.666	Putative
8	723	743	1.298	Certain
9	747	767	2.258	Certain
10	781	801	1.232	Certain
11	823	843	1.793	Certain
12	854	874	2.424	Certain
13	893	913	2.138	Certain

BLAST Alignment to Top Hit:

>CRA|18000005047237 /altid=gi|2498054 /def=sp|P70549|NAC3_RAT
SODIUM/CALCIUM EXCHANGER 3 PRECURSOR (NA+/CA2+-EXCHANGE
PROTEIN 3) /org=NA+/CA2+-EXCHANGE PROTEIN 3 /dataset=nraa
/length=927
Length = 927

Score = 1828 bits (4682), Expect = 0.0
Identities = 897/927 (96%), Positives = 911/927 (97%), Gaps = 6/927 (0%)
Frame = +1

```
Query: 10   MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 189
            MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAG   DVPS GQNNESCSGSSDCKEGVIL
Sbjct: 1    MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGDLRDVPSAGQNNESCSGSSDCKEGVIL 60

Query: 190  PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 369
            PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE
Sbjct: 61   PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120

Query: 370  TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 549
            TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI
Sbjct: 121  TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180

Query: 550  IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 729
            IIGICVYVIPDGETRKIKHLRVFF+TAAWS+FAYIWLYMILAVFSPGVVQVWEGLLTLFF
Sbjct: 181  IIGICVYVIPDGETRKIKHLRVFFVTAAWSVFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240

Query: 730  FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 909
            FPVCVLLAWVADKRLLFYKYMHK+YRTDKHRGIIIETEG+HPKGIEMDGKMMNSHFLDGN
Sbjct: 241  FPVCVLLAWVADKRLLFYKYMHKRYRTDKHRGIIIETEGEHPKGIEMDGKMMNSHFLDGN 300

Query: 910  LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 1089
            L+PLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR
Sbjct: 301  LIPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360

Query: 1090 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 1269
            MMTGAGNILKKHAAEQAKK +SMSEVHTDEPEDF SKVFFDPCSYQCLENCGAVLLTVVR
Sbjct: 361  MMTGAGNILKKHAAEQAKKTASMSEVHTDEPEDFASKVFFDPCSYQCLENCGAVLLTVVR 420

Query: 1270 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 1449
            KGGD+SKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF
Sbjct: 421  KGGDISKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480

Query: 1450 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 1629
            FVRLSNVR+EEEQ EEGM PAI NSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH
Sbjct: 481  FVRLSNVRVEEEQLEEGMTPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Query: 1630 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 1809
            VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV
Sbjct: 541  VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600

Query: 1810 KIVDEEEYERQENFFIALGEPKWMERGIS------DVTDRKLTMEEEEAKRIAEMGKPVL 1971
            KIVDEEEYERQENFFIALGEPKWMERGIS      +VTDRKLTMEEEEAKRIAEMGKPVL
Sbjct: 601  KIVDEEEYERQENFFIALGEPKWMERGISALLLSPEVTDRKLTMEEEEAKRIAEMGKPVL 660

Query: 1972 GEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 2151
            GEHPKLEVIIEESYEFK+TVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDE+EDESG
Sbjct: 661  GEHPKLEVIIEESYEFKSTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEEEDESG 720

Query: 2152 EERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFG 2331
            EERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACF VSILIIGMLTAIIGDLASHFG
Sbjct: 721  EERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFVVSILIIGMLTAIIGDLASHFG 780

Query: 2332 CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW 2511
            CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW
Sbjct: 781  CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW 840

Query: 2512 SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLA 2691
            SVAAIYWA+QGQEFHVSAGTLAFSVTLFTIFAFVC+SVLLYRRRPHLGGELGGPRGCKLA
Sbjct: 841  SVAAIYWAMQGQEFHVSAGTLAFSVTLFTIFAFVCLSVLLYRRRPHLGGELGGPRGCKLA 900
```

```
Query: 2692 TTWLFVSLWLLYILFATLEAYCYIKGF 2772
            TTWLFVSLWLLY+LFATLEAYCYIKGF
Sbjct: 901  TTWLFVSLWLLYVLFATLEAYCYIKGF 927 (SEQ ID NO:4)
```

Hmmer search results (Pfam):

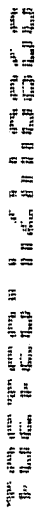
Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
PF01699	Sodium/calcium exchanger protein	294.6	1.2e-84	2
PF00324	Amino acid permease	2.8	5.9	1
PF01971	Protein of unknown function	2.7	8.7	1

Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t		score	E-value
PF01699	1/2	118	257	..	12	152	.]	121.3	1.8e-32
PF01971	1/1	644	670	..	193	222	..	2.7	8.7
PF00324	1/1	851	877	..	472	498	.]	2.8	5.9
PF01699	2/2	757	905	..	1	152	[]	181.4	1.5e-50

FIGURE 2, page 4 of 4



```
   1 TTGGATGAGA TCTAAAGCAT TATTAAGAGT GGGGAGTGCA AAGAAGAAAC
  51 CCTCATTTCA AAGATGAATG AGAATAATGG CATGTACAAA GGTCCTGGGG
 101 TGGACAGTCA CTTGGTATAA TCCAAGAGTG AACCTGAAGG CTATTGTTGT
 151 TGAAATGTAA TAAGGGAGAG AGTGACGGGA TGAAGGGGGA TGAGTGGGAA
 201 GCAGTGAATT CCTGCAAGGC TTTGAAGGTC ATGGGAAAGA ATTTGGTCTT
 251 TATATCAAGA GCAAGAGAAG ACTACTAAAG GGCTTCAAAC AGGGGAGCGA
 301 TATGCTTAAG TCTGTTTGTT TGTTTTTTTA AAAAAAGATT ACGGTGGCTA
 351 TATGAGGAAA GTGGAATTGA GAACTAGCGA GAGTTGGAGT GGTGAGCTCC
 401 ATTAGGAGGC TACTGAAGTA GATTCATGAG GTAAGGAGTG ATGGTGGCCT
 451 GGGCTGGGAT GATGGTGGTA GAAATGGAGA AAGAGTTGAT AGGATTTAGT
 501 GATTGGATAA GGGACAGAAG AGAGATGAAG GCTTTCAGAC TAACATCTGC
 551 TTTCTAACAT GAGTAACTGG GTGGCTGAAG ATGCTATTTT CTGAGCTGGG
 601 AAACAGGAGA AAAAGGAGCA AATATGGGGG ATGAAGACTT TGAGTCTTTA
 651 AGGTGCTGTA CAAACACAAA TCAGCATTCC TTTATTACTA AGGGTATCCC
 701 ACACAGTTGT AGCAGAGGGA GAAAGATCGC CCCCCCCCCA CTTTTTTTTT
 751 TTTTTTAGCT ATTCCATGGT ATTTTCATTC TCATCCCACC CAAATGAGGC
 801 AGTGAGTGGT AAGATGAGTA TATAATAGTT TCAATTGCAT TTCATCCCAT
 851 TCTTCTGAGC TCAAGCTCAC CTTTTAGTGG TTTGAGGCCA GTAGATGAAG
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 951 GAGACATTTG CATGTTTTAT TAATAATGAT TTTTACCACT TGTTCCTTTC
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1051 ACTGCCTGCT TAAACTGCTC ATAAGCAGGT TTTACTGGAG GGCTCAGAGC
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1451 CATTAAACAG AGCAAGGTTT TCAATTTTCT GGGGACTAGT CCATGAAAAT
1501 TCAATTCAAT ATACTCTCTT GCAAACCTAT GTTATCCAAG ATACTCAAGT
1551 ATAATGACAA CAGGGTAAGG AAGTCCGAAC ACCCCAGAAA CAGTATAAAT
1601 GGGCATGAAG ATTCAGGTTA TACATGGCCT ATTTTAAGTT GCTTCTTGAG
1651 AACTCTCACA GGTAATACCA GTTTGGGAGA CAGGACTTGA AGGCTATTGC
1701 TGCATTTCCA TCCCCAGTAT TCCCAGCTAT TTCAAGCCAT TTTTCAACGG
1751 AGTCTCCACC AGATGGTTTG GAGGACAGAG CAGCTATTTG TGCCTCCCAT
1801 TGACATCTAT TTTTCCAAGT GAGAGACTGC CCCATATGTT AGTGCAATAT
1851 GTCACTGGAG GTGAAGCATC AGTTGTATTG GTGGGAACCT GCCGTTTGCT
1901 GTCCCCTTTT TCCTCATGCC TTTTCCTGCC TCTCTGATCT TTTCTAGGTC
1951 TCTGGCCTAT CAGGAGGACA ACTGGTGCTG CAATAGAAGC CAGTGGCTAA
2001 GTCTCGTGTA TGGCGTGGTT AAGGTTGCAG CCTCTCACCT CTGCCTTCCT
2051 CCATTTTGGG CTGGTTACCT TTGTGCTCTT CCTGAATGGT CTTCGAGCAG
2101 AGGCTGGTGG CTCAGGGGAC GTGCCAAGCA CAGGGCAGAA CAATGAGTCC
2151 TGTTCAGGGT CATCGGACTG CAAGGAGGGT GTCATCCTGC CAATCTGGTA
2201 CCCGGAGAAC CCTTCCCTTG GGGACAAGAT TGCCAGGGTC ATTGTCTATT
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2801 GTACCGCACA GACAAACACC GAGGAATTAT CATAGAGACA GAGGGTGACC
2851 ACCCTAAGGG CATTGAGATG GATGGGAAAA TGATGAATTC CCATTTTCTA
2901 GATGGGAACC TGGTGCCCCT GGAAGGGAAG GAAGTGGATG AGTCCCGCAG
2951 AGAGATGATC CGGATTCTCA AGGATCTGAA GCAAAAACAC CCAGAGAAGG
3001 ACTTAGATCA GCTGGTGGAG ATGGCCAATT ACTATGCTCT TTCCCACCAA
3051 CAGAAGAGCC GCGCCTTCTA CCGTATCCAA GCCACTCGTA TGATGACTGG
3101 TGCAGGCAAT ATCCTGAAGA AACATGCAGC AGAACAAGCC AAGAAGGCCT
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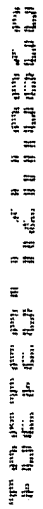

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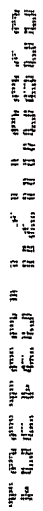

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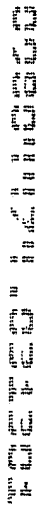

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FEATURES:

Start:	2010
Exon:	2010-3793
Intron:	3794-109509
Exon:	109510-109613
Intron:	109614-118338
Exon:	118339-118463
Intron:	118464-119345
Exon:	119346-119445
Intron:	119446-121409
Exon:	121410-121685
Intron:	121686-124128
Exon:	124129-124502
Stop:	124503

SNPs:

DNA Position	Major	Minor	Domain	Protein Position	Major	Minor
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742	T	-	Beyond ORF(5')			

2005	C	T	Beyond ORF(5')				
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122102	G	C	Intron
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124947	C	T	Beyond ORF(3')
125010	A	G	Beyond ORF(3')
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126283	C	G	Beyond ORF(3')

Context:

DNA
Position

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TGGAGGAAGGAGGTTTCTGTATCAGAAAGGCATTGGCCGTGACAGACTC

Chromosome map:
Chromosome 14